

6660843

FIG. 1

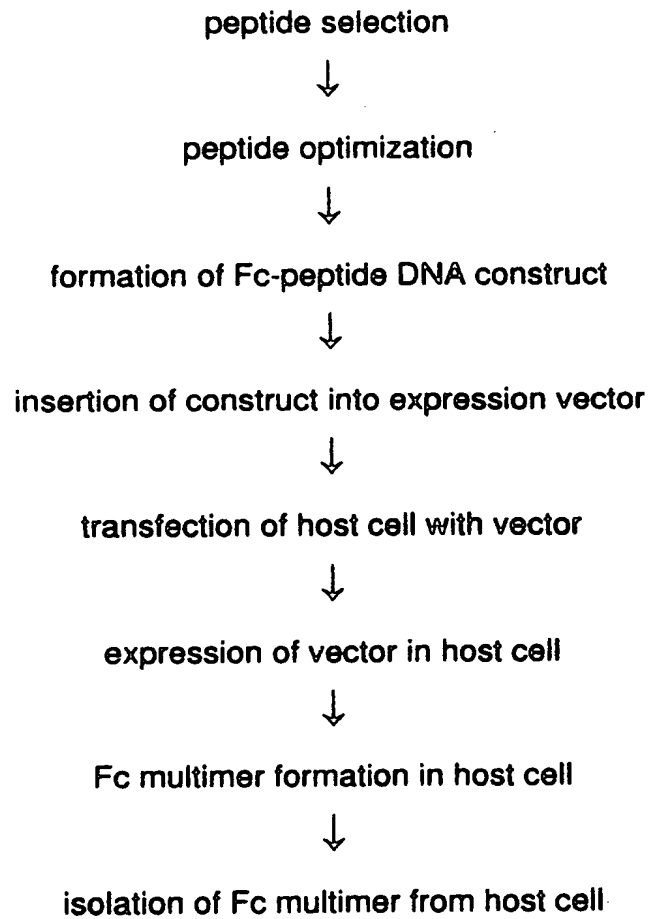


FIG. 2A

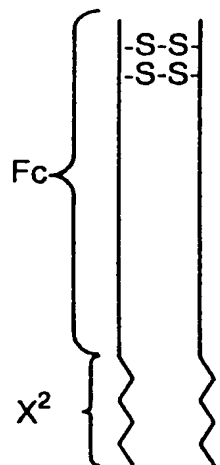


FIG. 2B

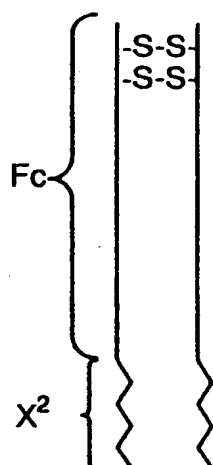


FIG. 2C

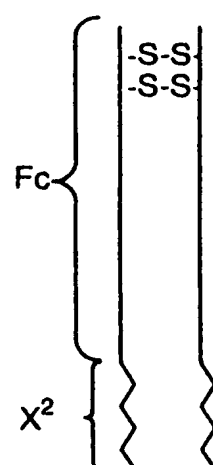


FIG. 2D

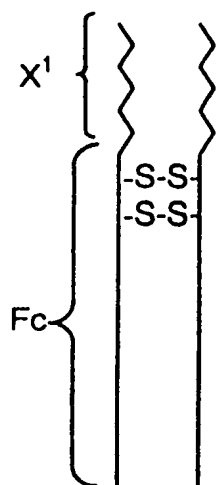


FIG. 2E

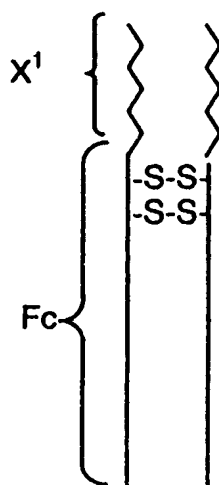
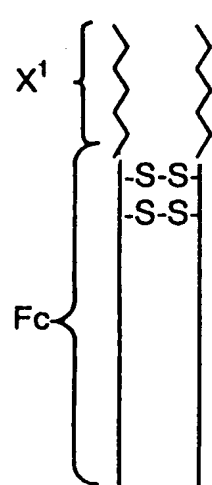


FIG. 2F



| | | |
|-----------|----------|--|
| APP | FIG. | |
| CLASS | SUBCLASS | |
| DRAFTSMAN | | |

FIG. 3A

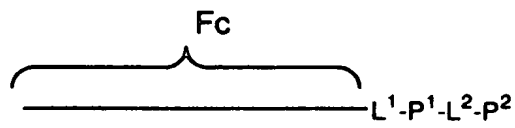


FIG. 3B

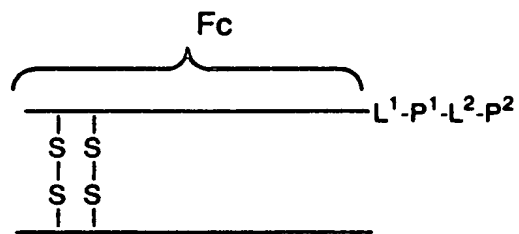


FIG. 3C

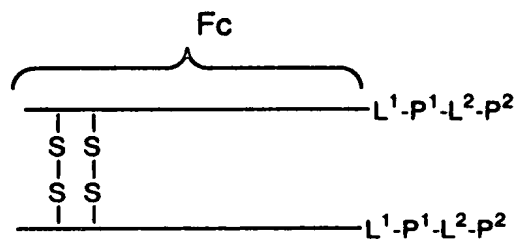


FIG. 4

```

ATGGACAAAAC TCACACATGTCCACCTTGTCCAGCTCCGGAAC TCCTGGGGGGACCGTCA
1  -----+-----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTTCGAGGCCTTGAGGACCCCCCTGGCAGT
a      M D K T H T C P P C P A P E L L G G P S -
GTCTTCCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTG
61  -----+-----+-----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG
a      V F L F P P K P K D T L M I S R T P E V -
ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121  -----+-----+-----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC
a      T C V V V D V S H E D P E V K F N W Y V -
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
181  -----+-----+-----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCGTTCGCGGCCCTCCTCGTCATGTTGTCGTGC
a      D G V E V H N A K T K P R E E Q Y N S T -
TACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241  -----+-----+-----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCTCATG
a      Y R V V S V L T V L H Q D W L N G K E Y -
AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
301  -----+-----+-----+-----+-----+-----+-----+-----+ 360
TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG
a      K C K V S N K A L P A P I E K T I S K A -
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
361  -----+-----+-----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG
a      K G Q P R E P Q V Y T L P P S R D E L T -
AAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTG
421  -----+-----+-----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC
a      K N Q V S L T C L V K G F Y P S D I A V -
GAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGTCTGGAC
481  -----+-----+-----+-----+-----+-----+-----+-----+ 540
CTCACCTCTCGTTACCCGTCGGCTCTTGTGATGTTCTGGTGCGGAGGGCACGACCTG
a      E W E S N G Q P E N N Y K T T P P V L D -
TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541  -----+-----+-----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTC
a      S D G S F F L Y S K L T V D K S R W Q Q -
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601  -----+-----+-----+-----+-----+-----+-----+-----+ 660
CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTC
a      G N V F S C S V M H E A L H N H Y T Q K -
AGCCTCTCCCTGTCTCCGGGTAAA
661  -----+-----+-----+-----+-----+-----+-----+-----+ 684
TCGGAGAGGGACAGAGGCCCATTT

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FIG. 5

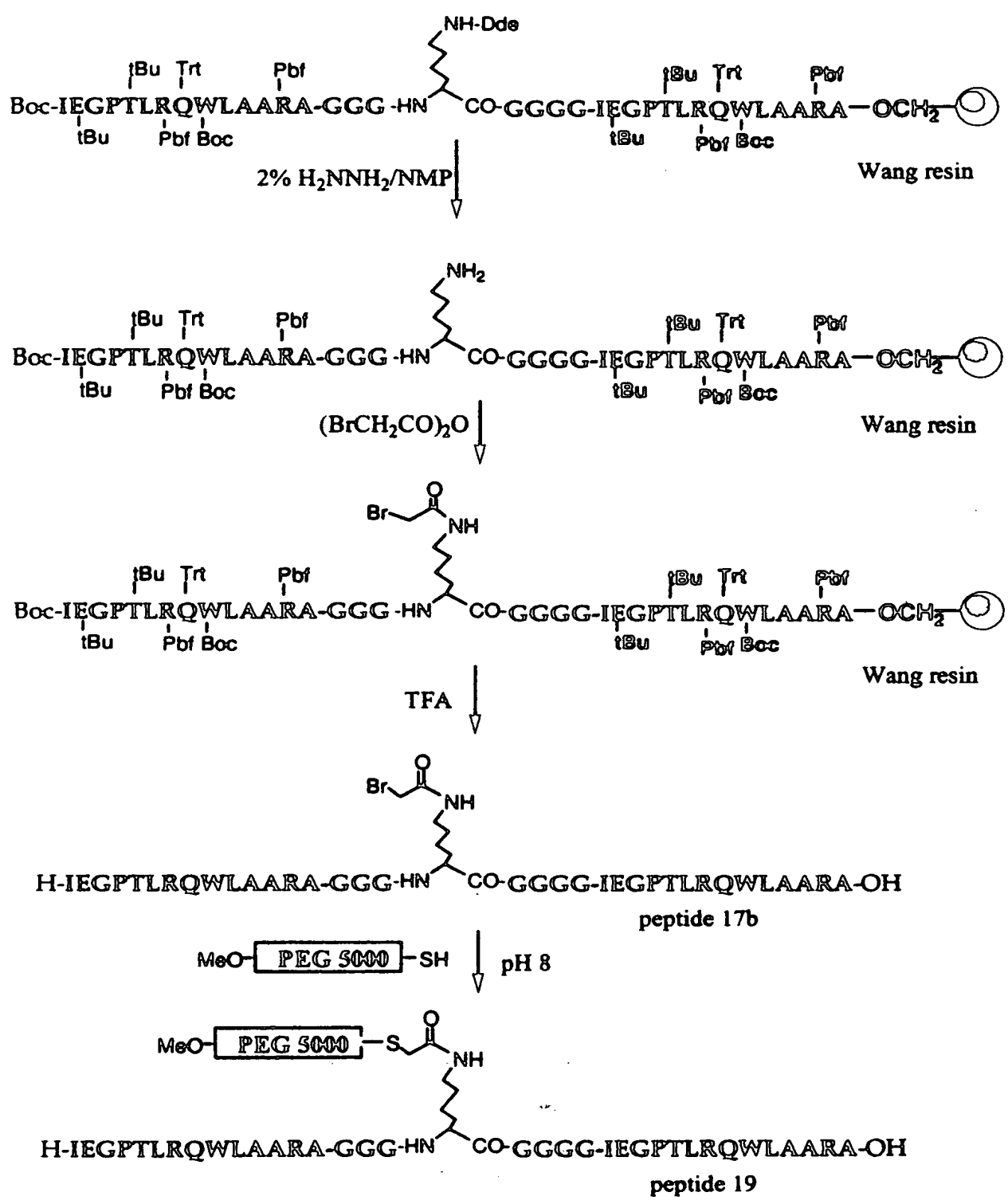


FIG. 6

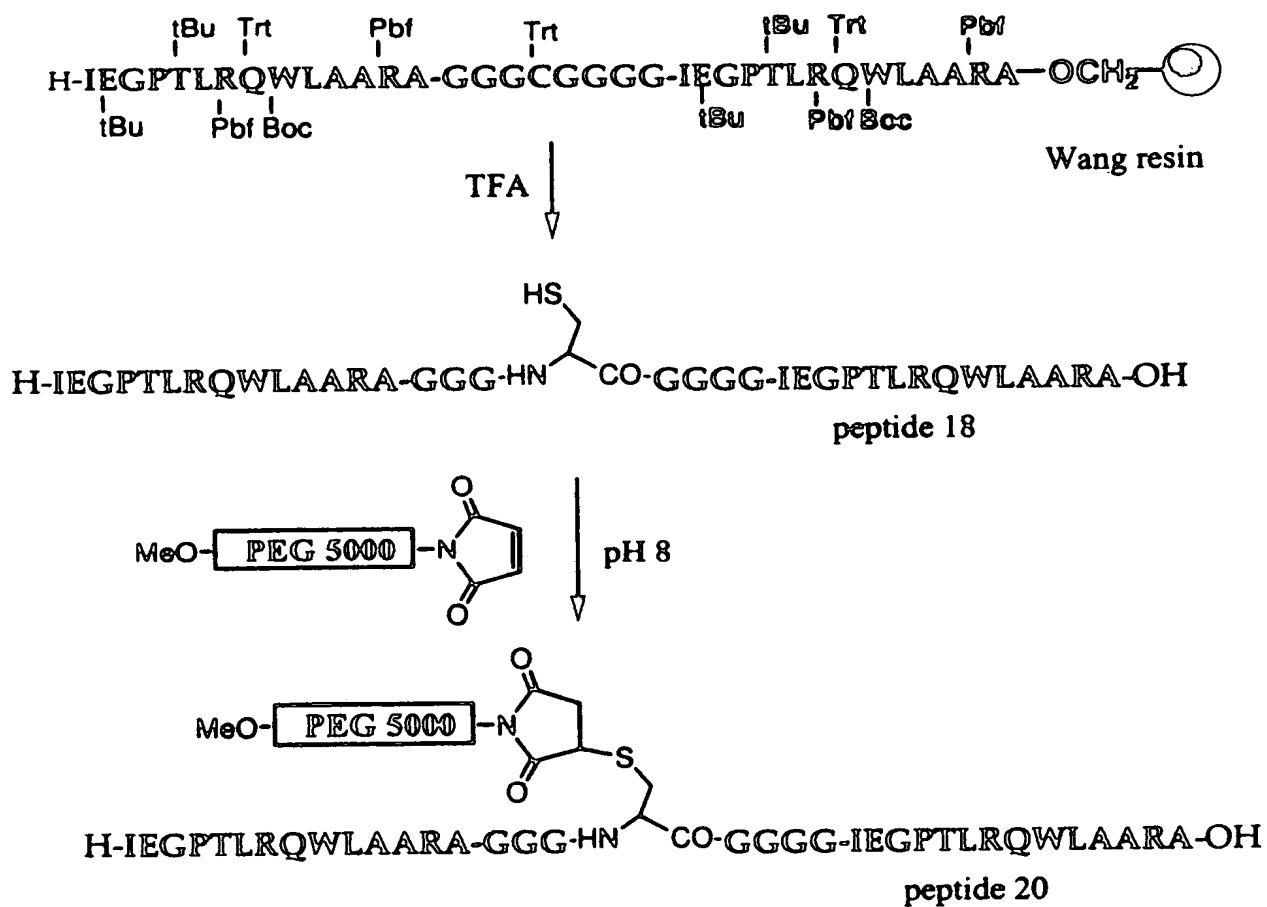


FIG. 7

XbaI
 |
 1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC 60
 AGATCTAAACAAAATTGATTAATTTCTCCTTATTGTATACCTGTTTGGAGTGTGTACAG
 M D K T H T C P
 C
 61 CACCTTGTCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC 120
 GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTTTG
 P C P A P E L L G G P S V F L F P P K P
 C
 121 CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGGACGTGA 180
 GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCAACCACTGCACT
 K D T L M I S R T P E V T C V V V D V S
 C
 181 GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240
 CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
 H E D P E V K F N W Y V D G V E V H N A
 C
 241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCA 300
 GGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTGTCGTGCATGGCACACCACTCGCAGGAGT
 K T K P R E E Q Y N S T Y R V V S V L T
 C
 301 CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG 360
 GGCAGGACGTGGTCTCTGACCGACTTACCGTTCTCTCATGTTTACGTTCCAGAGGTTGTTTC
 V L H Q D W L N G K E Y K C K V S N K A
 C
 361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420
 GGGAGGGTGGGGGTAGCTCTTTTGGTAGAGGTTTTCGGTTTCCCGTCGGGGCTCTTGGTG
 L P A P I E K T I S K A K G Q P R E P Q
 C
 421 AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT 480
 TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
 V Y T L P P S R D E L T K N Q V S L T C
 C
 481 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540
 CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG
 L V K G F Y P S D I A V E W E S N G Q P
 C
 541 CGGAGAACAACCTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCT 600
 GCCTCTTGTGTTGATGTTCTGCTGCGGAGGGCAGACCTGAGGCTGCCGAGGAAGAAGGAGA
 E N N Y K T T P P V L D S D G S F F L Y
 C
 601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660
 TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC
 S K L T V D K S R W Q Q G N V F S C S V
 C
 661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA 720
 ACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
 M H E A L H N H Y T Q K S L S L S P G K
 C
 721 AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTT 780
 TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGACGAGCACGAA
 G G G G G I E G P T L R Q W L A A R A *
 C
 BamHI
 |
 781 AATCTCGAGGATCC 794
 TTAGAGCTCCTAGG

FIG. 8

XbaI
 1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACACACATGTC
 AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
 M D K T H T C P
 61 CACCTTGTCCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC
 GTGGAACAGGTCGAGGCCTTGAGGACCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTG
 P C P A P E L L G G P S V F L F P P K P
 121 CCAAGGACACCCCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGGACGTGA
 GGTTCTGTGGGAGTACTAGAGGGCTGGGACTCCAGTGTACGCACCACACCTGCACCT
 K D T L M I S R T P E V T C V V V D V S
 181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
 CCGTGTCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
 H E D P E V K F N W Y V D G V E V H N A
 241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCA
 GGTTCTGTTCGGCGCCCTCCTCGTCATGTTGTGTCGTGCATGGCACACCACTCGCAGGAGT
 K T K P R E E Q Y N S T Y R V V S V L T
 301 CCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
 GGCAGGACGTGGTCTGACCGACTTACCGTTCTCTCATGTTCCAGTTCCAGAGGTTGTTTC
 V L H Q D W L N G K E Y K C K V S N K A
 361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
 GGGAGGGTCCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
 L P A P I E K T I S K A K G Q P R E P Q
 421 AGGTGTACACCCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCT
 TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGGA
 V Y T L P P S R D E L T K N Q V S L T C
 481 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
 CGGACCAGTTTCCGAAGATAGGGTGGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG
 L V K G F Y P S D I A V E W E S N G Q P
 541 CGGAGAACAACTACAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTCT
 GCCTCTTGTGATGTTCTGGTGGGAGGGACGACCTGAGGCTGCCGAGGAAGAAGGAGA
 E N N Y K T T P P V L D S D G S F F L Y
 601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
 TGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC
 S K L T V D K S R W Q Q G N V F S C S V
 661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
 ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCAT
 M H E A L H N H Y T Q K S L S L S P G K
 721 AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTG
 TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGACGACGACGAC
 G G G G G I E G P T L R Q W L A A R A G
 781 GTGGTGGAGGTGGCGGGGAGGTATTGAGGGCCCAACCCTTCGCCAATGGCTTGCAGCAC
 CACCACCTCCACCGCCGCTCCATAACTCCCGGGTGGGAAGCGGTTACCGAACGTCGTG
 G G G G G G I E G P T L R Q W L A A R
 BamHI
 841 GCGCATAATCTCGAGGATCCG
 CGCGTATTAGAGCTCCTAGGC

841 GTAAATAATGGATCC 855
-----+-----
CATTATTACCTAGG
K *

FIG. 10

FIG. 10

XbaI
|
TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
AGATCTAAACA AAAATTGATTAATTTCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG
M I E G P T L R -

GTCAGTGGCTGGCTGCTCGTGCTGGTGGAGGCCGTGGGGACAAAAC TCACACATGTCCAC
-----+-----+-----+-----+-----+-----+-----+-----+ 120
CAGTCACCGACCGACGAGCACGACCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG
Q W L A A R A G G G G G D K T H T C P P -

CTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTCTCTTCCCCCAAAACCCA
-----+-----+-----+-----+-----+-----+-----+-----+ 180
GAACGGGTCTGTTGACTTGAGGACCCCCCTGGCAGTCAAAGGAGAAGCGGGGTTTTGGGT
C P A P E L L G G P S V F L F P P K P K -

AGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCC
-----+-----+-----+-----+-----+-----+-----+-----+ 240
TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCCTCGG
D T L M I S R T P E V T C V V V D V S H -

ACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA
-----+-----+-----+-----+-----+-----+-----+-----+ 300
TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT
E D P E V K F N W Y V D G V E V H N A K -

AGACAAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCG
-----+-----+-----+-----+-----+-----+-----+-----+ 360
TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACAGTCCGAGGAGTGGC
T K P R E E Q Y N S T Y R V V S V L T V -

TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCC
-----+-----+-----+-----+-----+-----+-----+-----+ 420
AGGACGTGGTCTTGACCGACTTACCGTTCTCATGTTACGTTCCAGAGGTTGTTTCGGG
L H Q D W L N G K E Y K C K V S N K A L -

TCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
-----+-----+-----+-----+-----+-----+-----+-----+ 480
AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCGCTCGGGGCTCTTGGTGTCC
P A P I E K T I S K A K G Q P R E P Q V -

TGTACACCCTGCCCCCATCCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCC
-----+-----+-----+-----+-----+-----+-----+-----+ 540
ACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCCTTGGTCCAGTCGGACTGGACGG
Y T L P P S R D E L T K N Q V S L T C L -

TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
-----+-----+-----+-----+-----+-----+-----+-----+ 600
ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCC
V K G F Y P S D I A V E W E S N G Q P E -

AGAACA ACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACA
-----+-----+-----+-----+-----+-----+-----+-----+ 660
TCTTGTGTGATGTTCTGGTCCGGAGGGCAGCACCTGAGGCTGCCGAGGAAGAAGGAGATGT
N N Y K T T P P V L D S D G S F F L Y S -

GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGA
-----+-----+-----+-----+-----+-----+-----+-----+ 720
CGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGCACT
K L T V D K S R W Q Q G N V F S C S V M -

TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT
-----+-----+-----+-----+-----+-----+-----+-----+ 780
ACGTA CTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCCATTTA
H E A L H N H Y T Q K S L S L S P G K * -

BamHI
|
AATGGATCC
----- 789
TTACCTAGG

FIG.11

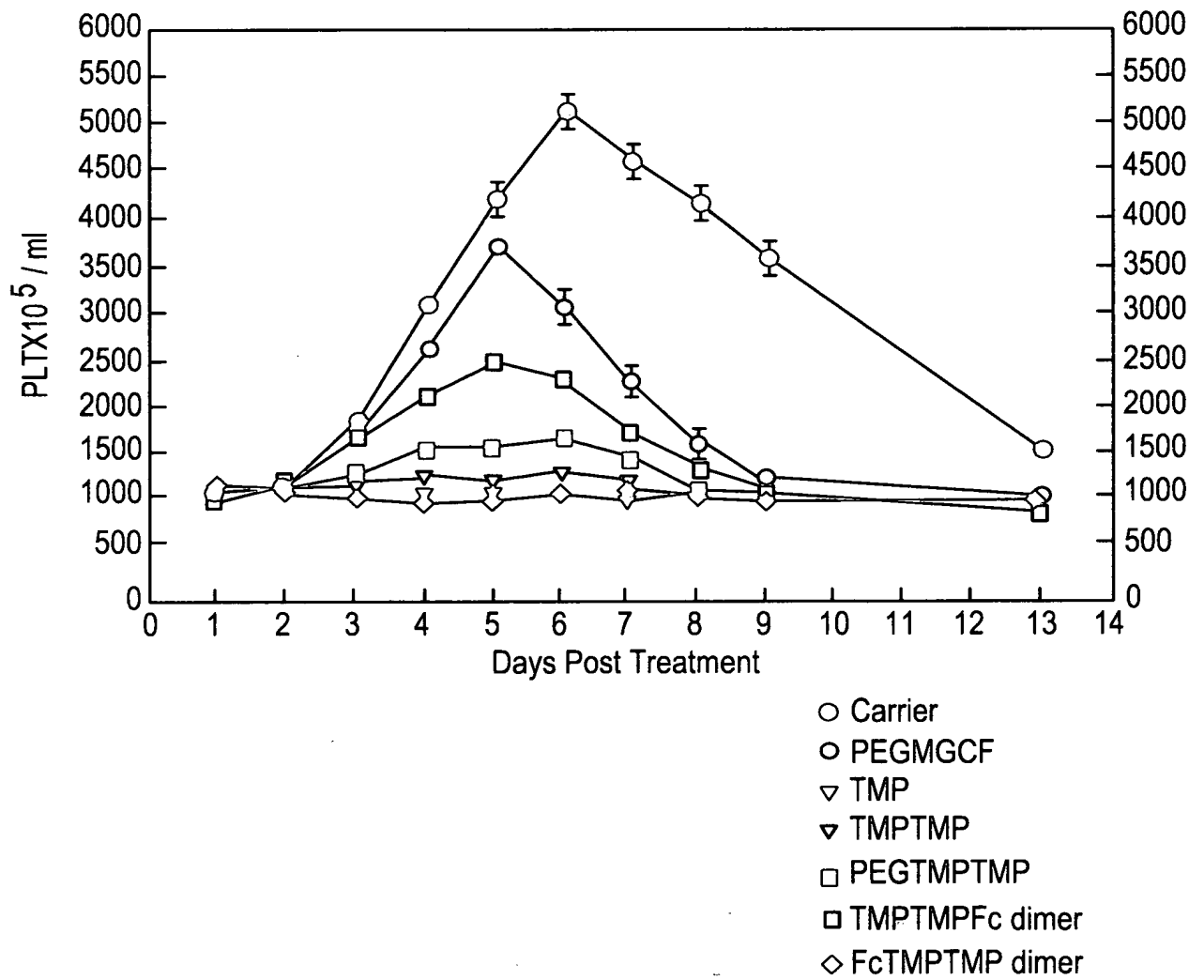


FIG.12

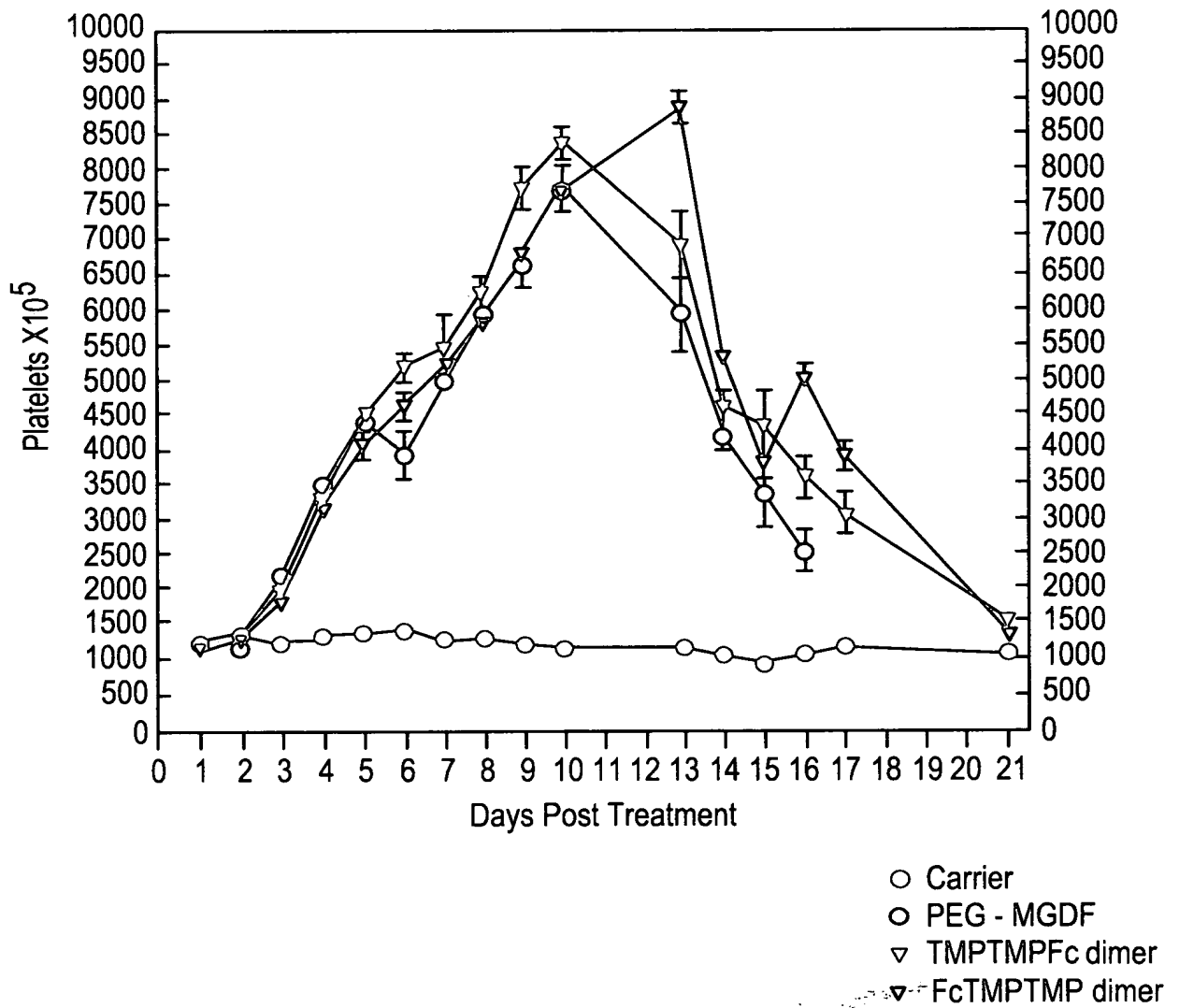


FIG. 13

XbaI
|
TCTAGATTGTTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACCTCACACATGTC
1+.....+.....+.....+.....+ 60
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG
.....+.....+.....+.....+.....+ M D K T H T C P -
CACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC
61+.....+.....+.....+.....+ 120
GTGGAACAGGTCGAGGCCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTTTG
P C P A P E L L G G P S V F L F P P K P -
CCAAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGA
121+.....+.....+.....+.....+ 180
GGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
K D T L M I S R T P E V T C V V V D V S -
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
181+.....+.....+.....+.....+ 240
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
H E D P E V K F N W Y V D G V E V H N A -
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCTCTCA
241+.....+.....+.....+.....+ 300
GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T -
CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
301+.....+.....+.....+.....+ 360
GGCAGGACGTGGTCTGACCGACTTACCGTTCTCATGTTTACGTTCCAGAGGTTGTTTC
V L H Q D W L N G K E Y K C K V S N K A -
CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
361+.....+.....+.....+.....+ 420
GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
L P A P I E K T I S K A K G Q P R E P Q -
AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTACAGCTGACCT
421+.....+.....+.....+.....+ 480
TCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
V Y T L P P S R D E L T K N Q V S L T C -
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
481+.....+.....+.....+.....+ 540
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG
L V K G F Y P S D I A V E W E S N G Q P -
CGGAGAACAACACTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCT
541+.....+.....+.....+.....+ 600
GCCTCTTGTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F F L Y -
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
601+.....+.....+.....+.....+ 660
TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGAGAAGAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V -
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
661+.....+.....+.....+.....+ 720
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
M H E A L H N H Y T Q K S L S L S P G K -
AAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCCGCTGACTTGGGTTT
721+.....+.....+.....+.....+ 780
TTCCACCTCCACCACCACCTCCATGAATGAGAACGGTGAAGCCGGGCGACTGAACCCAAA
G G G G G G G G T Y S C H F G P L T W V C -
BamHI
|
GCAAACCGCAGGGTGGTTAATCTCGTGATCC
781+.....+.....+.....+ 812
CGTTTGGCGTCCCAACCAATTAGAGCACCTAGG
K P Q G G *

FIG. 14

XbaI
|
1 TCTAGATTGTTTAACTAATTAAAGGAGGAATAACATATGGGAGGTACTTACTCTTGCC 60
AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCCTCCATGAATGAGAACGG
M G G T Y S C H
c
61 ACTTCGGCCCCGCTGACTTGGGTATGTAAGCCACAAGGGGGTGGGGGAGGCGGGGGGACA 120
TGAAGCCGGGCGACTGAACCCATACATTGGGTGTTCCCCCACCCTCCGCCCCCTGT
F G P L T W V C K P Q G G G G G G D K
c
121 AAATCACACATGTCCACCTTGCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTTC 180
TTTGAGTGTGTACAGGTGGAACGGGTGCTGGACTTGAGGACCCCTGGCAGTCAAAGG
T H T C P P C P A P E L L G G P S V F L
c
181 TCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTACATGCG 240
AGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGG
F P P K P K D T L M I S R T P E V T C V
c
241 TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 300
ACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGC
V V D V S H E D P E V K F N W Y V D G V
c
301 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG 360
ACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCAC
E V H N A K T K P R E E Q Y N S T Y R V
c
361 TGGTCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA 420
ACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCCTTCTCATGTTTCACGT
V S V L T V L H Q D W L N G K E Y K C K
c
421 AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGC 480
TCCAGAGGTTGTTTCGGGAGGGTTCGGGGTAGCTCTTTGGTAGAGGTTTCGGTTTCCCG
V S N K A L P A P I E K T I S K A K G Q
c
481 AGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACC 540
TCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTCTTGG
P R E P Q V Y T L P P S R D E L T K N Q
c
541 AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG 600
TCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCC
V S L T C L V K G F Y P S D I A V E W E
c
601 AGAGCAATGGGCAGCCGGAACAACATAAGACCACGCCTCCCGTGCTGGACTCCGACG 660
TCTCGTTACCCGTGGCCTCTTGTGATGTTCTGGTGGGAGGGCAGACCTGAGGCTGC
S N G Q P E N N Y K T T P P V L D S D G
c
661 GCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG 720
CGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGC
S F F L Y S K L T V D K S R W Q Q G N V
c
721 TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT 780
AGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGA
F S C S V M H E A L H N H Y T Q K S L S
c
BamHI
|
781 CCCTGTCTCCGGGTAAATAATGGATCC 807
GGGACAGAGGCCCATTTATTACCTAGG
L S P G K *

FIG. 15

XbaI

TCTAGATTTTGAAGTTTAATAACTTTTGTAGAAGGAGGAATAAAATATGGGAGGTACTTACTCTTG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
AGATCTAAACTCAAAATTGAAAATCTTCCTCCTTATTTTTATACCCTCCATGAATGAGAAC
M G G T Y S C -

CCACTTCGGCCCCACTGACTTTGGGTTTGCAAACCGCAGGGTGGCGGCCGGCGGC GGCTGG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
GGTGAAGCCGGGTGACTGAACCCAACGTTTGGCGTCCCACCGCCGCCCGCCGCCACCC
H F G P L T W V C K P Q G G G G G G G G G -

TACCTATTCTGTCTATTTTGGCCCCGCTGACCTGGGTATGTAAGCCACAAGGGGGTGGGGG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
ATGGATAAGGACAGTAAAACCGGGCGACTGGACCCATACATTCCGTGTTCCCCCACCCCC
T Y S C H F G P L T W V C K P Q G G G G G -

AGGCGGGGGGGACAAAACCTCACACATGTCCACCTTGCCAGCACCTGAACTCCTGGGGGG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
TCCGCCCCCCTGTTTGTAGTGTTGACAGGTGGAACGGTCTGGACTTGAGGACCCCC
G G G D K T H T C P P C P A P E L L G G -

ACCGTCAGTTTTCTCTTCCCCC AAAACCAAGGACACCCTCATGATCTCCCGGACCCC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
TGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCTGGGG
P S V F L F P P K P K D T L M I S R T P -

TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
ACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGAC
E V T C V V V D V S H E D P E V K F N W -

GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
CATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCAATGT
Y V D G V E V H N A K T K P R E E Q Y N -

CAGCACGTACCGTGTGGTCAGCGTCTCACCGTCTGCAACCAGGACTGGCTGAATGGCAA
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
GTCGTGCATGGCACACCAAGTGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTT
S T Y R V V S V L T V L H Q D W L N G K -

GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
CCTCATGTTACGTTTCCAGAGGTTGTTTCCGGAGGGTCCGGGGTAGCTCTTTTGGTAGAG
E Y K C K V S N K A L P A P I E K T I S -

CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGATGA
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
GTTTCGGTTTCCCGTCCGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACT
K A K G Q P R E P Q V Y T L P P S R D E -

GCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
CGACTGGTTCTTGGTCCAGTCCGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTA
L T K N Q V S L T C L V K G F Y P S D I -

CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATACAAGACCACGCCTCCCGT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
GCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGTATGTTCTGGTGGGAGGGCA
A V E W E S N G Q P E N N Y K T T P P V -

GCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTGTTTCGAGTGGCACCTGTTCTCGTCCAC
L D S D G S F F L Y S K L T V D K S R W -

GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
CGTCGTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTATGT
O O G N V F S C S V M H E A L H N H Y T -

BathHI

GCAGAAGAGCCTCTCCCTGTCTCCGGTAAATAAT^TGATCC
841 -----+-----+-----+-----+ 881
CGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
O K S L S L S P G K *

FIG. 16

XbaI

1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACCTCACACATGTC 60

AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG

M D K T H T C P

61 CACCTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTCTCTTCCCCCAAAAC 120

GTGGAACGGTTCGTGGACTTGAGGACCCCTGGCAGTCAAAGGAGAAGGGGGTTTTG

P C P A P E L L G G P S V F L F P P K P

121 CCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA 180

GGTTCCTGTGGGAGTACTAGAGGGCCTGGGACTCCAGTGTACGCACCAACCTGCACT

K D T L M I S R T P E V T C V V V D V S

181 GCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240

CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC

H E D P E V K F N W Y V D G V E V H N A

241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCTCA 300

GGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTGTCGTGCATGGCACACCACTGCGAGGAGT

K T K P R E E Q Y N S T Y R V V S V L T

301 CCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG 360

GGCAGGACGTGGTCTGACCGACTTACCGTTCTCATGTTACGTTCCAGAGGTGTTTC

V L H Q D W L N G K E Y K C K V S N K A

361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420

GGGAGGGTTCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG

L P A P I E K T I S K A K G Q P R E P Q

421 AGGTGTACACCCTGCCTCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT 480

TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCCGACTGGA

V Y T L P P S R D E L T K N Q V S L T C

481 GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540

CGGACCAGTTTCCGAAGATAGGGTCGTGTAGCGGCACCTCACCTCTCGTTACCCGTG

L V K G F Y P S D I A V E W E S N G Q P

541 CGGAGAACAACCTACAAGACACGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCT 600

GCCTCTTGTGATGTTCTGGTGGGAGGGCAGACCTGAGGCTGCCGAGGAAGAAGGAGA

E N N Y K T T P P V L D S D G S F F L Y

601 ACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660

TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCTTGCAGAAGAGTACGAGGC

S K L T V D K S R W Q Q G N V F S C S V

661 TGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTA 720

ACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGACAGAGGCCAT

M H E A L H N H Y T Q K S L S L S P G K

721 AAGGTGGAGGTGGTGGCGGAGGTACTTACTCTTGCCACTTCGGCCCACTGACTTGGGTTT 780

TTCCACCTCCACCACCGCCTCCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCAAA

G G G G G G G T Y S C H F G P L T W V C

781 GCAAACCGCAGGTGGCGGCGGCGGCGGCGGTGGTACCTATTCTGTCAATTTGGCCCGC 840

CGTTTGGCGTCCACCGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG

K P Q G G G G G G G G T Y S C H F G P L

BamHI

841 TGACCTGGGTATGTAAGCCACAAGGGGTTAATCTCGAGGATCC 884

ACTGGACCCATACATTGGGTGTTCCCCCAATTAGAGCTCCTAGG

T W V C K P Q G G

FIG. 17A

[AatII sticky end] 5' GCGTAACGTATGCATGGTCTCC-
(position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

-CCATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-
-GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGA-
-GGGCCTTTTCGTTTTATCTGTTGTTTGTCTGGTGAACGCTCTCCTGAGTAGGACAAATCCGC-
-CCCGGAAAGCAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCTGTTTAGGCG-
-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCCG-
-GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCCCTCCACCGCCCGTCTGCGGGCG-
-CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCTGACGGATGGCCTTTTTTGCGT-
-GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA-
AatII
-TTCTACAACTCTTTTGTATTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC-
-AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG-
-TTTTAAAGTATGGGCAATCAATTGCTCCTGTAAATTTGCTTTAGAAATACTTTGGCAGC-
-AAAATTTTATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG-
-GGTTTGTGTTGATTTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC-
-CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCACGCGAATG-
-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCTTCGTCATGCCCACGCTAAAC-
-ATGTCGGATTATAAAAACTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG-
-ATTCTTTTTCTCTTTTGGTTAAATCGTTGTTTGATTTATTATTTGCTATATTTATTTTTC-
-TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAAG-
-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTATACACGCATGTAAAAATA-
-CTATTAATAGTTGATCTCTTCTTGTAAATTACCATAACAAGTATGTGCGTACATTTTTAT-
-AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAACTAAGCATTCCGAAGCCATTAT-
-TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTGTAAGGCTTCGGTAATA-
-TAGCAGTATGAATAGGGAACTAAACCCAGTGATAAGACCTGATGATTTGCTTCTTTAA-
-ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT-
-TTACATTTGGAGATTTTTTATTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG-
-AATGTAAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC-
-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT-
-TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-
-AATATTGCCTCCATTTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-
-TTATAACGGAGGTAAAAAATCCCATTAATAGGTCTTAACCTTTATAGTCTAAATTGGTATC-
-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG-
-TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAATCAGTATAGTC-
-ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT-
-TATTCGTAACATAATTATAGTAATAACGAAGATGTCCGAAATTAAAAATAATTAATAAGACA-
-AAGTGTCGTCGGCATTATGTCTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTG-
-TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-
-GCAAGTTTTGCGTGTTATATATCATTAAACGGTAATAGATTGACATTTGATTCTAATAA-
-CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT-

FIG. 17B

- ATTGGATTTTTGTCACACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG -
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTAAACAAATTGTATTCATGGAC -
- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT -
- ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -
- CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -
- GATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT -

- GCTCACTAGTGTGCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -

- GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -
- CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -

- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGG -
- TGATCGTATTGGGGAACCCCGGAGATTGCCCAGAACTCCCCAAAAACGACTTTCCTCC -

- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]
- TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)

FIG.18A - 1

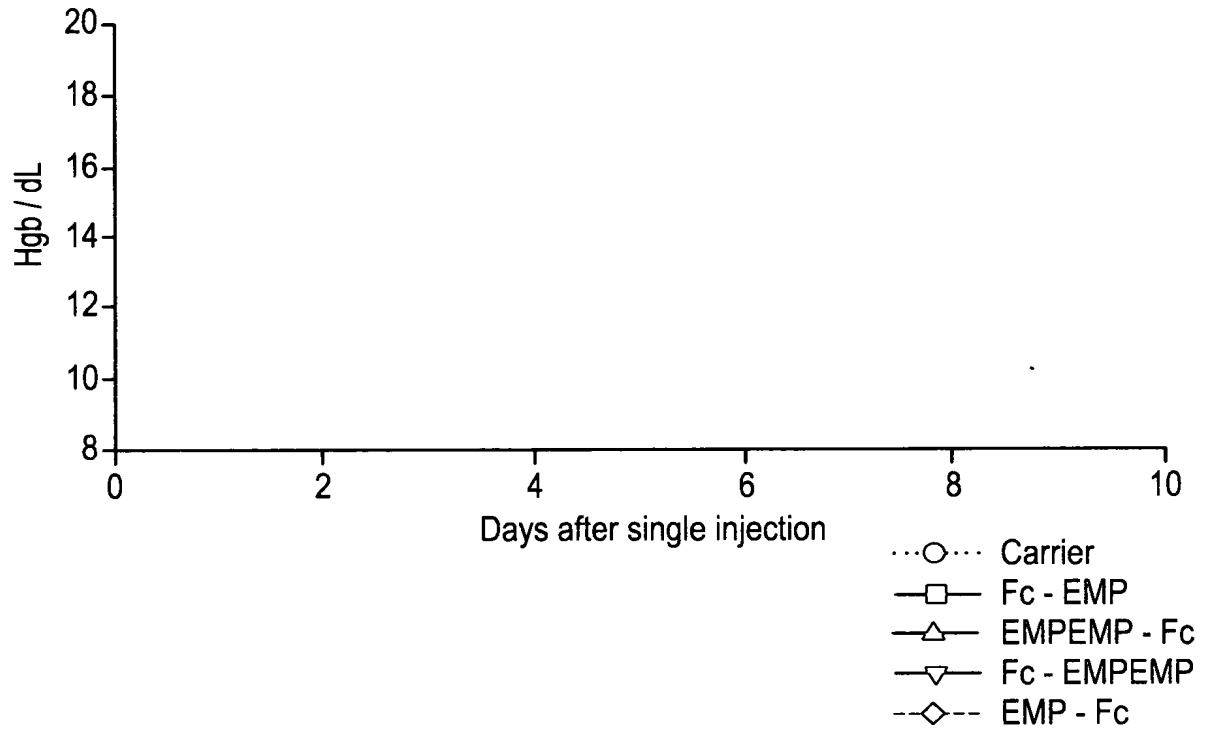


FIG.18A - 2

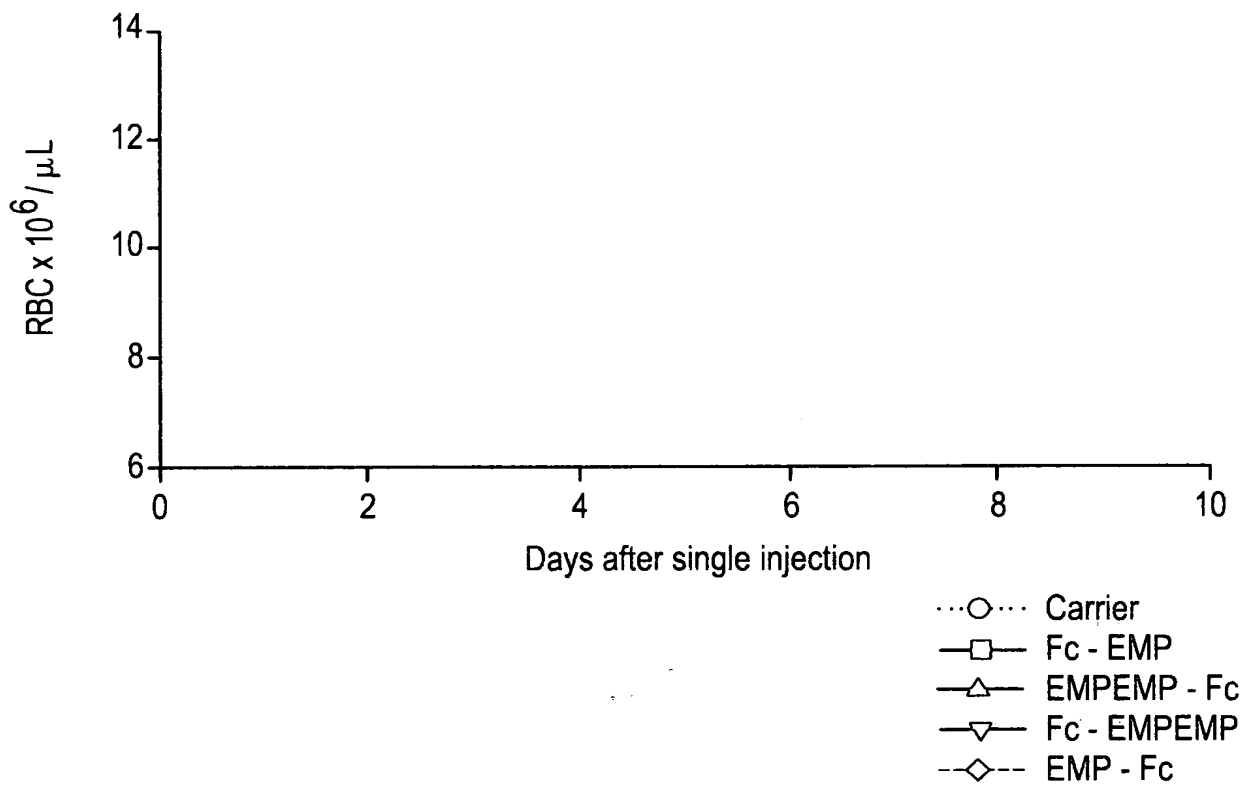


FIG.18A - 3

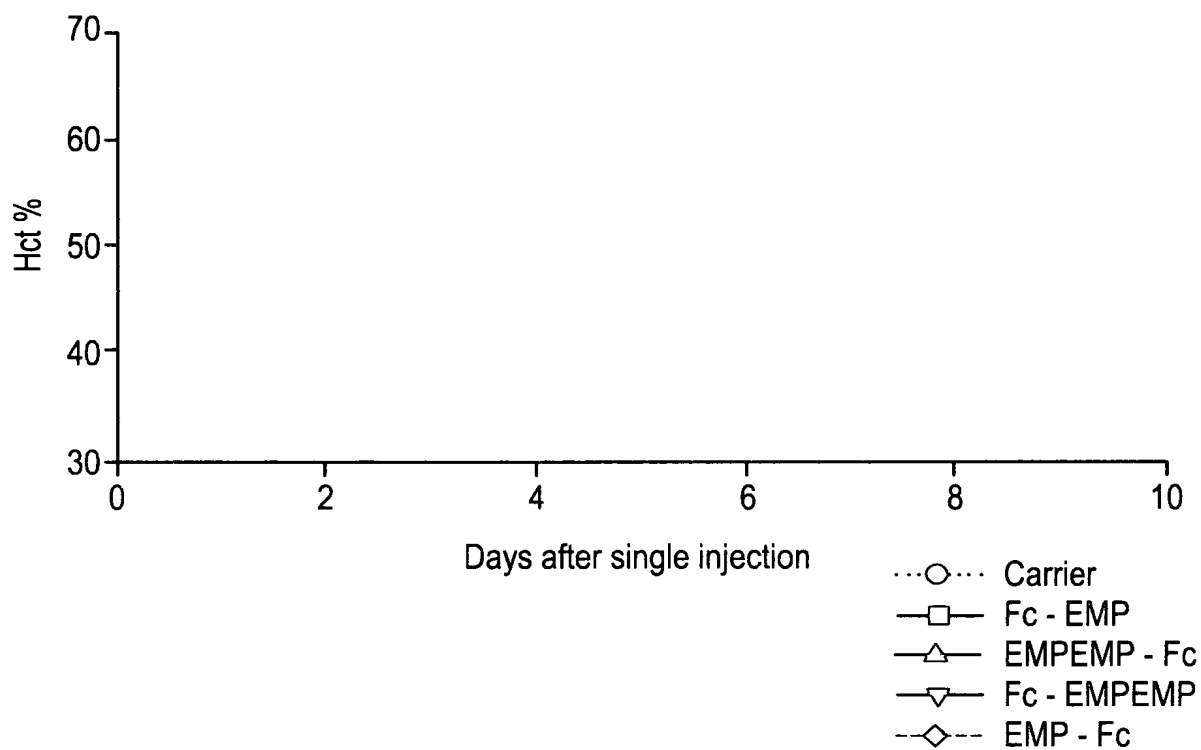


FIG.18B - 1

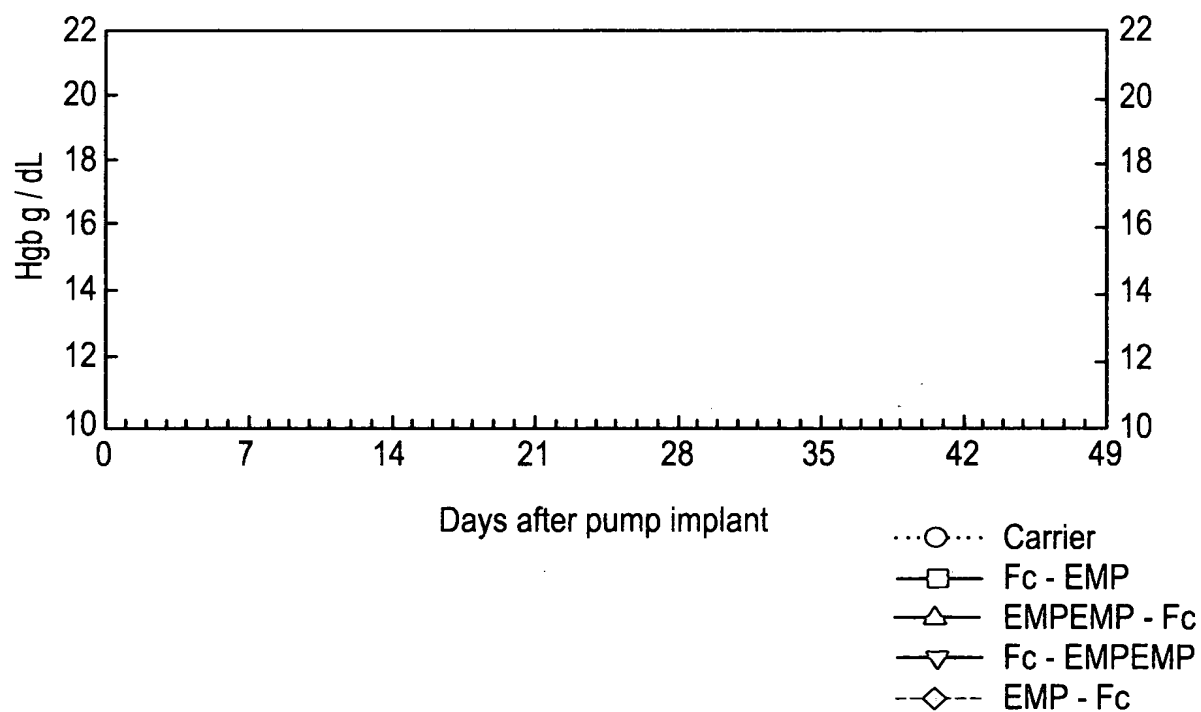


FIG.18B - 2

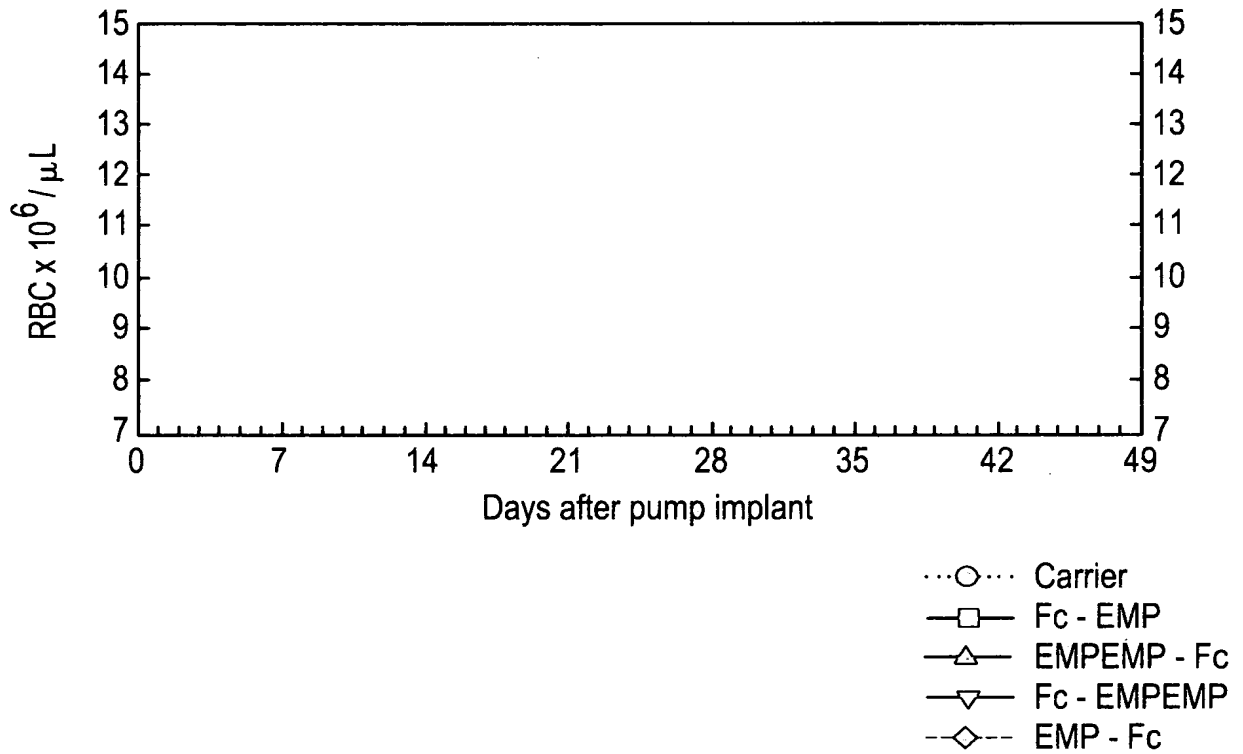


FIG.18B - 3

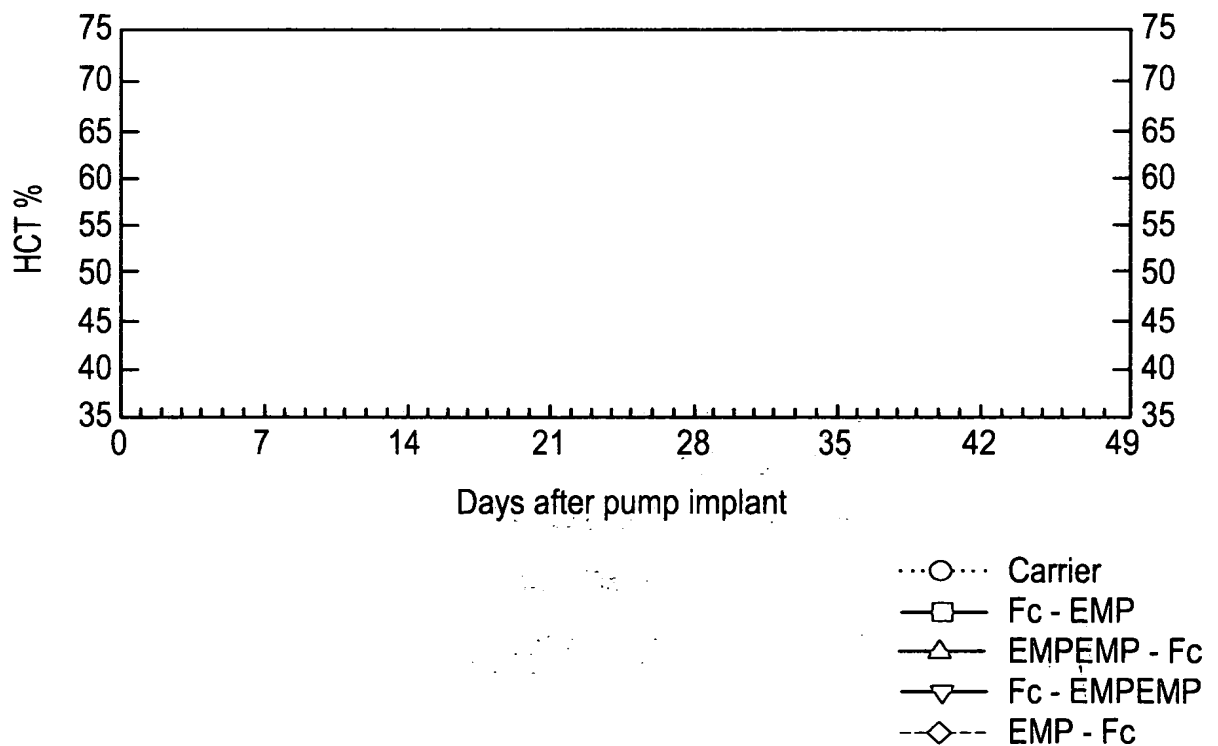


FIG. 19A

NdeI

1
 CATATGGACAAAACCTCACACATGTCCACCTTGTCAGCTCCGGAACCTCTGGGGGGACCG
 -----+-----+-----+-----+-----+-----+-----+ 60
 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61
 TCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
 -----+-----+-----+-----+-----+-----+-----+ 120
 AGTCAGAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121
 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
 -----+-----+-----+-----+-----+-----+-----+ 180
 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181
 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
 -----+-----+-----+-----+-----+-----+-----+ 240
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG

a V D G V E V H N A K T K P R E E Q Y N S -

241
 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
 -----+-----+-----+-----+-----+-----+-----+ 300
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301
 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
 -----+-----+-----+-----+-----+-----+-----+ 360
 ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

361
 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
 -----+-----+-----+-----+-----+-----+-----+ 420
 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421
 ACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC
 -----+-----+-----+-----+-----+-----+-----+ 480
 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481
 GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACTACAAGACCACGCCTCCCGTGCTG
 -----+-----+-----+-----+-----+-----+-----+ 540
 CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

541
 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
 -----+-----+-----+-----+-----+-----+-----+ 600
 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

| | |
|-----------|----------|
| AF | FIG. |
| CLASS | SUBCLASS |
| DRAFTSMAN | |

FIG. 19B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC
-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG

a   K   S   L   S   L   S   P   G   K   G   G   G   G   G   D   F   L   P   H   Y   -

                                     BamHI
                                     |
721 AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC
-----+-----+-----+-----+ 757
TTTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG

a   K   N   T   S   L   G   H   R   P   *

```


| | |
|-----------|----------|
| APP | FIG. |
| CLASS | SUBCLASS |
| DRAFTSMAN | |

FIG. 20B

601 GACTCCGACGGCTCCTTCTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
+.....+.....+.....+.....+.....+.....+ 660
 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
+.....+.....+.....+.....+.....+.....+ 720
 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a Q G N V F S C S V M H E A L H N H Y T Q -

BamHI

721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG
+.....+.....+.....+.....+.....+ 761
 TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC

a K S L S L S P G K *

FIG. 21A

NdeI
 |
 1 CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCG 60
 -----+-----+-----+-----+-----+-----+-----+
 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTTCGAGGCCCTGAGGACCCCCCTGGC
 a M D K T H T C P P C P A P E L L G G P -
 61 TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
 -----+-----+-----+-----+-----+-----+-----+
 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC
 a S V F L F P P K P K D T L M I S R T P E -
 121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
 -----+-----+-----+-----+-----+-----+-----+
 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
 a V T C V V V D V S H E D P E V K F N W Y -
 181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
 -----+-----+-----+-----+-----+-----+-----+
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC
 a V D G V E V H N A K T K P R E E Q Y N S -
 241 ACGTACCGTGTGGTCAGCGTCCTCACCCTGCTGACCAGGACTGGCTGAATGGCAAGGAG 300
 -----+-----+-----+-----+-----+-----+-----+
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTC
 a T Y R V V S V L T V L H Q D W L N G K E -
 301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
 -----+-----+-----+-----+-----+-----+-----+
 ATGTTTACGTTCCAGAGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
 a Y K C K V S N K A L P A P I E K T I S K -
 361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
 -----+-----+-----+-----+-----+-----+-----+
 CGGTTTCCCGTCCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
 a A K G Q P R E P Q V Y T L P P S R D E L -
 421 ACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC 480
 -----+-----+-----+-----+-----+-----+-----+
 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
 a T K N Q V S L T C L V K G F Y P S D I A -
 481 GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACTACAAGACCACGCCTCCCGTGCTG 540
 -----+-----+-----+-----+-----+-----+-----+
 CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGGGAGGGCAGGAC
 541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
 -----+-----+-----+-----+-----+-----+-----+
 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
 a D S D G S F F L Y S K L T V D K S R W Q -

| | |
|-----------|----------|
| APR 1980 | FIG. |
| CLASS | SUBCLASS |
| DRAFTSMAN | |

FIG. 21B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA

a   K   S   L   S   L   S   P   G   K   G   G   G   G   G   F   E   W   T   P   G   -

                                     BamHI
                                     |
721 TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
-----+-----+-----+-----+ 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC

a   Y   W   Q   P   Y   A   L   P   L   *
```

FIG. 22A

NdeI
|
1 CATATGTTTGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC 60
-----+-----+-----+-----+-----+-----+-----+
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG
a M F E W T P G Y W Q P Y A L P L G G G -
61 GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG 120
-----+-----+-----+-----+-----+-----+-----+
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTTCGTGGACTTGAGGACCCCCCTGGC
a G G D K T H T C P P C P A P E L L G G P -
121 TCAGTTTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 180
-----+-----+-----+-----+-----+-----+-----+
AGTCAAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
181 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 240
-----+-----+-----+-----+-----+-----+-----+
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
241 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 300
-----+-----+-----+-----+-----+-----+-----+
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGCG
a V D G V E V H N A K T K P R E E Q Y N S -
301 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 360
-----+-----+-----+-----+-----+-----+-----+
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
361 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 420
-----+-----+-----+-----+-----+-----+-----+
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
421 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 480
-----+-----+-----+-----+-----+-----+-----+
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
481 ACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 540
-----+-----+-----+-----+-----+-----+-----+
TGGTTCCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
541 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCTCCCGTGCTG 600
-----+-----+-----+-----+-----+-----+-----+
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -

| | |
|-----------|----------|
| APPENDIX | FIG. |
| CLASS | SUBCLASS |
| DRAFTSMAN | |

FIG. 22B

```

601  GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+-----+-----+ 660
      CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a      D S D G S F F L Y S K L T V D K S R W Q -

      CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
661  -----+-----+-----+-----+-----+-----+ 720
      GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
      AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721  -----+-----+-----+-----+-----+ 757
      TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG

a      K S L S L S P G K *

```

FIG. 23A

NdeI
|

```

1  CATATGGACAAAACCTCACACATGTCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCG
   -----+-----+-----+-----+-----+-----+-----+
a  M D K T H T C P P C P A P E L L G G P -

61 TCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
   -----+-----+-----+-----+-----+-----+-----+
a  S V F L F P P K P K D T L M I S R T P E -

121 AGTCAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC
   -----+-----+-----+-----+-----+-----+-----+
a  V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
   -----+-----+-----+-----+-----+-----+-----+
a  V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
   -----+-----+-----+-----+-----+-----+-----+
a  T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA
   -----+-----+-----+-----+-----+-----+-----+
a  Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
   -----+-----+-----+-----+-----+-----+-----+
a  A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
   -----+-----+-----+-----+-----+-----+-----+
a  T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTG
   -----+-----+-----+-----+-----+-----+-----+
a  V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
   -----+-----+-----+-----+-----+-----+-----+
a  D S D G S F F L Y S K L T V D K S R W Q -

581 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
   -----+-----+-----+-----+-----+-----+-----+
a  D S D G S F F L Y S K L T V D K S R W Q -

```

FIG. 23B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGGTGAACCGAACTGTGAC 720
-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACCTGGCTTGACACTG

a   K   S   L   S   L   S   P   G   K   G   G   G   G   G   V   E   P   N   C   D   -

                                     BamHI
                                     |
721 ATCCATGTTATGTGGAATGGGAATGTTTTGAACGTCTGTAACTCGAGGATCC 773
-----+-----+-----+-----+-----+
TAGGTACAATACACCCTTACCCTTACAAAACCTGCAGACATTGAGCTCCTAGG

a   I   H   V   M   W   E   W   E   C   F   E   R   L   *
```

FIG. 24A

NdeI
|
CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACCTTGCA

a M V E P N C D I H V M W E W E C F E R -

CTGGGTGGTGGTGGTGGTGACAAAACCTCACACATGTCCACCGTGCCAGCACCTGAACTC
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
GACCCACCACCACCACCACTGTTTTGAGTGTGTACAGGTGGCAGGGTCGTGGACTTGAG

a L G G G G G D K T H T C P P C P A P E L -

CTGGGGGGACCGTCAGTTTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCC
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
GACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGG

a L G G P S V F L F P P K P K D T L M I S -

CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAG
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC

a R T P E V T C V V V D V S H E D P E V K -

TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC

a F N W Y V D G V E V H N A K T K P R E E -

CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTTGACCGAC

a Q Y N S T Y R V V S V L T V L H Q D W L -

AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
TTACCGTTCCTCATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT

a N G K E Y K C K V S N K A L P A P I E K -

ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG

a T I S K A K G Q P R E P Q V Y T L P P S -

CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGG

a R D E L T K N Q V S L T C L V K G F Y P -

AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACG
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC

a S D I A V E W E S N G Q P E N N Y K T T -


```

601 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCCTCTACAGCAAGCTCACCGTGGACAAG
-----+-----+-----+-----+-----+-----+-----+ 660
GGAGGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTC

P P V L D S D G S F F L Y S K L T V D K -

661 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
-----+-----+-----+-----+-----+-----+ 720
TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG

S R W Q Q G N V F S C S V M H E A L H N -

BamHI
      |
721 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC
-----+-----+-----+-----+-----+-----+ 773
GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG

H Y T Q K S L S L S P G K *

```

FIG. 25A

NdeI
|
CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCG
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTTCGAGGCCTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
TCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
61 -----+-----+-----+-----+-----+-----+-----+ 120
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
121 -----+-----+-----+-----+-----+-----+-----+ 180
CAGTGACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCTCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
301 -----+-----+-----+-----+-----+-----+-----+ 360
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
361 -----+-----+-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAACAACACTACAAGACCACGCCTCCCGTGCTG
481 -----+-----+-----+-----+-----+-----+-----+ 540
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

| | | |
|----------|-----------|----------|
| PPROJ. | FIG. FIG. | |
| BY | CLASS | SUBCLASS |
| RAFTSMAN | | |

FIG. 25B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   -

AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCCACTGGGGT
661 -----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA

A   K   S   L   S   L   S   P   G   K   G   G   G   G   G   C   T   T   H   W   G   -

                                     BamHI
                                     |
TTCACCCTGTGCTAATGGATCCCTCGAG
721 -----+-----+-----+-----+ 748
AAGTGGGACACGATTACCTAGGGAGCTC

a   F   T   L   C   *
```

FIG. 26A

NdeI
|

```

1  CATATGTGCACCACTGGGGTTTCACCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT 60
   +-----+-----+-----+-----+-----+-----+
a  M C T T H W G F T L C G G G G G D K G -
   GGAGGCGGTGGGGACAAACTCACACATGTCCACCTTGCCAGCACCTGAACTCCTGGGG
61 +-----+-----+-----+-----+-----+-----+ 120
   CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCTGGAAGTGGAGGACCC
a  G G G G D K T H T C P P C P A P E L L G -
   GGACCGTCAGTTTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACC
121 +-----+-----+-----+-----+-----+-----+ 180
   CCTGGCAGTCAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG
a  G P S V F L F P P K P K D T L M I S R T -
   CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
181 +-----+-----+-----+-----+-----+-----+ 240
   GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG
a  P E V T C V V V D V S H E D P E V K F N -
   TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC
241 +-----+-----+-----+-----+-----+-----+ 300
   ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG
a  W Y V D G V E V H N A K T K P R E E Q Y -
   AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC
301 +-----+-----+-----+-----+-----+-----+ 360
   TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG
a  N S T Y R V V S V L T V L H Q D W L N G -
   AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATC
361 +-----+-----+-----+-----+-----+-----+ 420
   TTCCTCATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG
a  K E Y K C K V S N K A L P A P I E K T I -
   TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT
421 +-----+-----+-----+-----+-----+-----+ 480
   AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA
a  S K A K G Q P R E P Q V Y T L P P S R D -
   GAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
481 +-----+-----+-----+-----+-----+-----+ 540
   CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTG
a  E L T K N Q V S L T C L V K G F Y P S D -
   ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCC
541 +-----+-----+-----+-----+-----+-----+ 600
   TAGCGGCACCTCACCCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCAGGGG
a  I A V E W E S N G Q P E N N Y K T T P P -

```

| | |
|-----------|----------|
| APP | FIG. |
| CLASS | SUBCLASS |
| DRAFTSMAN | |

FIG. 26B

```

601 GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG
-----+-----+-----+-----+-----+-----+-----+ 660
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCC

a      V L D S D G S F F L Y S K L T V D K S R -

661 TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
-----+-----+-----+-----+-----+-----+ 720
ACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG

a      W Q Q G N V F S C S V M H E A L H N H Y -

                                           BamHI
                                           |
721 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
-----+-----+-----+-----+-----+ 763
TGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG

a      T Q K S L S L S P G K *
```

FIG. 2A

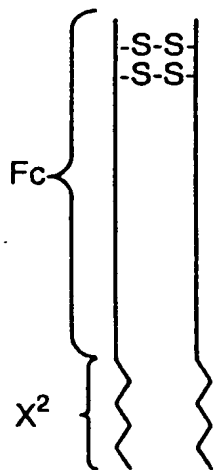


FIG. 2B

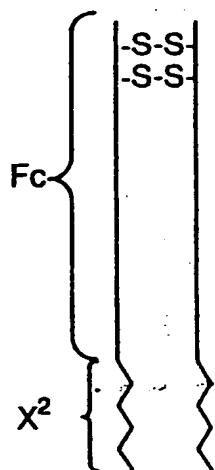


FIG. 2C

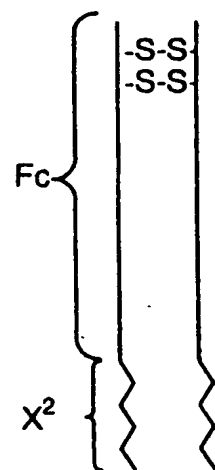


FIG. 2D

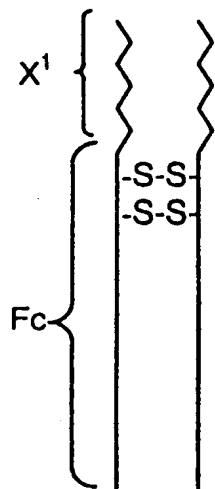


FIG. 2E

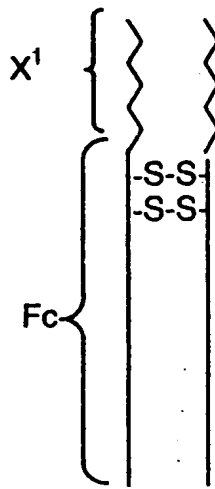


FIG. 2F

